The earth is home for all kinds of living organisms, whose genetic diversity and relationships with their physical environment constitute biodiversity. Biodiversity or biological diversity generally refers to the variability among living organisms from all sources including, *inter alia*, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are a part; this includes diversity within species, between species and of ecosystems. It plays fundamental roles in maintaining and enhancing the well-being of the world’s more than 6.7 billion people and it comprises much of the renewable natural capital on which livelihoods and development are grounded.

India is a major centre of origin and diversity of crop and medicinal plants. It holds an extraordinary significance among the top gene-rich countries of the world relating to its abundantly rich land race diversity in agricultural and horticultural crops and their wild relatives. India has four global biodiversity hot spots. The Western Ghats is one among them which posses very rich in its medicinal wealth. The forests and hills of this region is a treasure house of about 700 medicinal plants, out of which some are used for traditional and folk medicinal practices.

Due to the rising of international demand, many important medicinal plant species are becoming scarce and some are facing the prospect of extinction. Therefore it is important to conserve the extensively used and traded medicinal plants in its natural environment or cultivating it in favorable environments. Conservation of plant genetic diversity is an essential component of the sustainability of the ecosystem and for the human well being.
Genetic diversity is at the lowest hierarchy, without genetic diversity, a population cannot evolve and adapt to environmental changes. But genetic diversity has an impact on the higher levels of biodiversity. Analysis of genetic structure at intra specific level of medicinal plant species is important to development of conservation strategies, exploration of plant genetic resources and future breeding programs of wild plants.

Various types of markers such as morphological, chromosomal, biochemical and molecular markers are used for this purpose. DNA based markers provide new tool for ecological process. Newer markers provide more detailed genetic information to either the increased variability of loci or the greater number of the available loci. These markers have successfully been used to estimate levels of relatedness among the individuals, studies of mating systems, and of seed dispersal and seedling establishment in natural population.

Random Amplified Polymorphic DNA and Inter Simple Sequence Repeats are extensively used to evaluate DNA polymorphism. There techniques help researches not only to identifying the genotypes but also in assessing and exploiting genetic variability of medicinal species like *Plumbago zeylanica* L. and *Withania somnifera* (L) Dunal. The study of genetic diversity of chosen medicinal plants using molecular markers is needed to determine the superiority of the species. This work needed and it is going to be useful to the medicinal practitioners and in vitro culture for mass propagation.

Plant samples of *Plumbago zeylanica* L. and *Withania somnifera* (L.) Dunal were collected from five geographically distinct locations for the present study. Fresh and healthy young leaf samples were randomly collected from its natural population. The collected plant samples were put in zip - lock plastic bags with silica gel and transported to
laboratory. The samples were maintained in deep freezer at -70°C. The identification of specimens was confirmed by comparing them with authentic specimens available in herbarium of Botanical Survey of India (BSI), Coimbatore and St. Xavier’s College Herbarium (XCH), Palayamkottai. The voucher specimens of the samples were deposited in the Herbarium of St. Xavier’s College, Palayamkottai, Tamilnadu, India.

The morphological features of the chosen plants were observed during the field study and soil samples were collected for the analysis of pH, Micronutrients, Macronutrients and Organic contents.

The modified Midiprep method was followed for the isolation of genomic DNA from *P. zeylanica* and *W. somnifera*. The DNA was assessed by UV-VIS spectrophotometer in order to find out the purity and the quantity of the DNA for RAPD and ISSR analysis. Primers which produced reproducible bands were selected for RAPD and ISSR analysis. The data was interpreted using NTSYS and POPGENE software, package.

The study area presents a whole range of gradients, both altitudinal as well as latitudinal in climatic factors, such as total annual rainfall, maximum temperatures were observed. Distinct variations were observed in the soil samples analyzed. Distinct morphological variations were observed in each samples collected from different locations.

The genetic diversity was assessed by RAPD in *P. zeylanica* and their number of amplified DNA fragments varied from 7 to 13. The total number of amplified fragments was 128. Overall genetic diversity or heterozygosity was 0.34 and the highest percentage
of polymorphism (89.38 %) was observed in the species of *P. zeylanica* collected from Kallar (Ooty).

RAPD was used to analyze the genetic diversity in *W. somnifera* and their number of amplified DNA fragments varied from 5 to 9. The total number of amplified fragments was 78. Overall genetic diversity or heterozygosity was 0.2892 and the highest percentage of polymorphism (84.62 %) was observed in the species of *W. somnifera* collected from Hosur (Krishnagiri).

The genetic variability was evaluated in *P. zeylanica* using ISSR and their number of amplified DNA fragments varied from 4 to 7. The total number of amplified fragments was 68. Overall genetic diversity or heterozygosity was 0.2353 and the highest percentage of polymorphism (70.59 %) was observed in the species of *P. zeylanica* collected from Kallar (Ooty).

The genetic diversity was assessed by ISSR in *W. somnifera* and their number of amplified DNA fragments varied from 4 to 9. The total number of amplified fragments was 65. Overall genetic diversity or heterozygosity was 0.1945 and the highest percentage of polymorphism (66.15 %) was observed in the species of *W. somnifera* collected from Hosur (Krishnagiri).

The present findings, comparing the soil factors of five accessions of *P. zeylanica*, it is found that the sandy clay loamy soil in the characteristic of five localities (Kallar, Senkottai gap, Oothu, Palagat Gap and Aralvoimozhi). The pH was high in oothu accessions when compared to other accession. The amount of macronutrients N (126
kg/acre), P (30 kg/acre) and the K (345 kg/acre) was high in PZ₁ location collected from Kallar (Ooty) in the Western Ghats of south India. The altitude of these accession was 8° 11´04 N (Latitude) and 76° 07´ E (Longitude). The rate of rainfall in the year 2008 and 2009 of Kallar accession was high (440 mm) in October 2008 and low (1.7 mm) in January 2009. Among the accession studied P. zeylanica collected from the Kallar accession is considered as the superior genotype due to the soil characters, rate of rainfall and high percentage of polymorphism in RAPD (86.38) and ISSR (70.59).

In the present study the soil characteristic of W. somnifera showed that it is grown on different nature of soil. Sandy clay loam soil is the characteristics of five accessions of Thirukurankudi, Megamalai, Vellayangiri, Hosur and Chamrajnagar were found. The pH was high in Vellayangiri accessions when compared to other accession. The amount of macronutrients N (99kg/acre), P (25 kg/acre) and the K (500 kg/acre) was high in WS₄ location collected from Hosur in the Western Ghats of south India. The altitude of these accession was 12° 30´ N (Latitude) and 76° 65´ E (Longitude). The rate of rainfall in the year 2008 and 2009 of Hosur accession was 283.8 mm in September 2009, low (0.4 mm) in January 2009. Among the accession studied W. somnifera collected from the Hosur accession is the superior genotype due to the soil characters, rate of rainfall and high percentage of polymorphism in RAPD (84.62) and ISSR (66.15).

Significant correlation was observed with regard to genetic diversity and soil factors of each species collected from different geographical locations. Thus, in the present study, the population which exhibited high percentage of polymorphism was considered to be the superior genotypes.
This study revealed that RAPD and ISSR technique are very effective in determining the genetic diversity. It is also concluded that the genetic variability is influenced by phytogeographical, environmental and edaphic factors. In future, the superior genotypes of these medicinal plants can be collected and mass propagated through micropropagation and the active principles can be extracted in large quantities through phytochemical analysis for various medicinal uses. Such superior genotypes may be introduced into different areas of the forest as one of the methods of species recovery programme and it can also be recommended to the pharmaceutical industries and to the medicinal practitioners for the formulation of drug.